AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 15, line 15 and ending on page 17, line 4 with the following rewritten paragraph:

In a third approach, the assay distinguishes the fragment (or fragments) based on one or more epitopes in thrombospondin that are not present in the fragment. As an illustrative but not restrictive example, an epitope shared by thrombospondin and a thrombospondin fragment is used to obtain a quantitation of a total, thrombospondin plus thrombospondin fragment (s), from which is then subtracted a quantitation of thrombospondin obtained using an epitope present in thrombospondin but not present in a fragment. The difference between the two quantitations is a quantitation of the amount of fragment. As an example, epitopes in thrombospondin but not in at least one fragment from the group of an 80 to 100 kDa, a 40 to 55 kDa, or a 20 to 35 kDa fragment present in plasma can be selected from the group consisting of an epitope from outside the protease-resistant central core domain, an epitope in the N-terminal domain, an epitope in the N-terminal heparin-binding domain, a heparin- binding sequence in the N-terminal domain, a heparin-binding sequence in the N-terminal domain selected from the group consisting of residues 23-32 (RKGSGRRLVK SEQ ID NO: 59), residues 23- 29 (RKGSGRR SEQ ID NO: 60), and residues 77-83 (RQMKKTR SEQ ID NO: 61) of the mature protein (see Chapter 2, "The primary structure of the thrombospondins"in The Thrombospondin Gene Family by JC Adams, RP Tucker, & J Lawler, Springer-Verlag: New York, 1995, pp. 11-42, but especially p. 13 & Table 2.1 ; Chapter 6, "Mechanistic and functional aspects of the interactions of thrombospondins with cell surfaces,"ibidem pp. 105-157, but especially pp. 108 & 114; Lawler J et al. Expression and mutagenesis of thrombospondin. Biochemistry. 1992 Feb 4; 31 (4): 1173-80; and Cardin AD & Weintraub HJ. Molecular modeling of protein- glycosaminoglycan interactions. Arteriosclerosis. 1989 Jan-Feb ; 9 (1) : 21-32), a heparin- binding sequence in the N-terminal domain selected from the group consisting of residues 22-29 (ARKGSGRR (SEQ ID NO: 62)), residues 79-84 (MKKTRG (SEQ ID NO: 63)), and residues 178-189 (RLRIAKGGVNDN (SEQ ID NO: 64)) of the mature protein (reviewed in the Discussion section of Voland C et al.: Platelet-osteosarcoma cell interaction is mediated through a specific

fibrinogen- binding sequence located within the N-terminal domain of thrombospondin 1. J Bone Miner Res. 2000 Feb; 15 (2): 361-368), an epitope in the C-terminal domain, an epitope in the C-terminal cell-binding domain, a thrombospondin epitope not found in a plasma fragment, a thrombospondin epitope not found in a plasma fragment of 80 to 100 kDa, a thrombospondin epitope not found in a plasma fragment of 40 to 55 kDa, and a thrombospondin epitope not found in a plasma fragment of 20 to 35 kDa, where all kDa molecular weights are those after reduction. It is understood that the absence of a strong, functional heparin-binding domain from a thrombospondin fragment in plasma will be a factor allowing its accumulation in plasma (many heparin-or heparan-binding proteins are cleared from plasma very quickly ; see for example, Wallinder L et al. Rapid removal to the liver of intravenously injected lipoprotein lipase. Biochim Biophys Acta. 1979 Oct 26; 575 (1) : 166-73).

Please replace the paragraph beginning on page 25, line 6 and ending on page 25, line 20, with the following rewritten paragraph:

Raising conventional antibodies (also referred to herein simply as "antibodies" as opposed to "single chain antibodies" ; and an example of a conventional antibody is IgG, which is composed of two heavy chains and two light chains) is merely one of a number of methods that are generally based on the approach of random, semi-random, directed, combinatorial, and/or other means for the generation of large numbers of diverse peptides and/or non-peptides, that is then followed by a selection procedure to identify within this large number those peptides and/or non-peptides that bind to a target and/or an epitope within a target. Selection can then be followed by methods for improving the peptides and/or non-peptides to achieve better affinity and/or specificity. These diverse peptides and/or non-peptides may be conventional multi-chain antibodies (polyclonal or monoclonal), single-chain antibodies, or non-antibodies, including but not limited to peptides, products of phage display, aptamers, DNA, RNA, or modified DNA or RNA. Also contemplated are thrombospondin receptors and/or binding proteins (such as a CSVTCG (SEQ ID NO: 54) receptor, a CSVTCG (SEQ ID NO: 54) binding molecule, CD36,

angiocidin, 26S proteasome non-ATPase regulatory subunit 4, and/or anti-secretory factor).

Please replace the paragraph beginning on page 32, line 8 and ending on page 32, line 16, with the following rewritten paragraph:

Such kits wherein said protein non-antibody is selected from the group consisting of a thrombospondin receptor, a thrombospondin receptor that binds within a protease-resistant core region, a thrombospondin receptor that binds a TSP fragment present in the plasma of a cancer patient, a CSVTCG (SEQ ID NO: 54) receptor, a CSVTCG (SEQ ID NO: 54) binding molecule, a CD36 (which reportedly binds CSVTCG (SEQ ID NO: 54); see Carron JA et al. , A CD36-binding peptide from thrombospondin-1 can stimulate resorption by osteoclasts in vitro. Biochem Biophys Res Commun. 2000 Apr 21; 270 (3): 1124-7), angiocidin, anti-secretory factor, 26S proteasome non-ATPase regulatory subunit 4, fragments thereof that bind to their respective targets, and combinations, chimeras, and recombinant versions of said receptors and fragments.

Please replace the paragraph beginning on page 44, line 9 and ending on page 45, line 11, with the following rewritten paragraph:

It is believed that the-85 kDa,-50 kDa, and-30 kDa fragments all contain an immunogenic portion of "collagen type V-binding domain "of thrombospondin. In a preferred aspect of the invention, the fragments are detected by antibody that binds to such a domain, as is believed to be the case for the TSP Ab-4 monoclonal antibody referred to below. Because the collagen V-binding domain is relatively small (-19 kDa; see Takagi et al. JBC 1993), it is concluded from the apparent molecular weights of these fragments, which are substantially greater than 19kDa, that additional portions of the thrombospondin molecule must also be present in these fragments (multimers of the 19-kDa region are not a plausible explanation for the higher molecular weights, because the 19-kDa region does not comprise the region of inter-chain disulfide bonds,

plus the fact that the gels in Figures 3 and 4 were run under reducing conditions). It is believed that additional portions come from the protease-resistant central core domain of thrombospondin, which can be selected from the group of thrombospondin domains consisting of the region of inter-chain disulfide bonds, the procollagen-like domain, a type 1 repeat, and to some extent a type 2 repeat and a type 3 repeat (see Prater CA et al. The properdin-like type 1 repeats of human thrombospondin contain a cell attachment site. J Cell Biol. 1991 Mar; 112 (5): 1031-40; Schultz-Cherry S et al.

The type 1 repeats of thrombospondin 1 activate latent transforming growth factor-beta. J Biol Chem. 1994 Oct 28; 269 (43): 26783-8 ; Figure 6.2 in Adams JC et al. The Thrombospondin Gene Family, 1995, p. 107; and chymotryptic and tryptic fragments of thrombospondin indicated schematically in Figure 1 of this application). See also the sequence ranges given earlier in this Application. Note that several aforementioned peptides, such as, CNSPSPQMNGKPCEGEAR (SEQ ID NO: 8) (residues 444-461), RKVTEENKELANELRPP (SEQ ID NO: 9) residues 281-297) ; PQMNGKPCEGEAR (SEQ ID NO: 11) (residues 449-461); CEGEAR (SEQ ID NO: 12) (residues 456-461; and RKVTEENKE (SEQ ID NO: 13) (residues 281-289) are within the protease- resistant central core domain. An antibody against a region outside of a collagen V-binding domain, but present in a thrombospondin fragment present in a cancer patient, is also preferred.